RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:	10/747,702	
Source:	IFNO	
Date Processed by STIC:	10-07-2005	

ENTERED



IFWO

RAW SEQUENCE LISTING DATE: 10/07/2005 PATENT APPLICATION: US/10/747,702 TIME: 12:54:20

```
1 <110> APPLICANT: Ahmad, Sultan
             Banville, Denis
              Fortin, Yves
     3
             Lembo, Paola
      5
              O'Donnell, Dajan
              Shi-Hsiang, Shen
      7 <120> TITLE OF INVENTION: G Protein-Coupled Receptors from the Rat and Human
      8 <130> FILE REFERENCE: 81823/268117
      9 <140> CURRENT APPLICATION NUMBER: US/10/747,702
C--> 10 <141> CURRENT FILING DATE: 2003-12-30
    11 <150> PRIOR APPLICATION NUMBER: PRIO APPLICATION NUMBER: US/09/254,227
     12 <151> PRIOR FILING DATE: 1999-03-03
     13 <160> NUMBER OF SEQ ID NOS: 22
     14 <170> SOFTWARE: PatentIn version 3.0
     16 <210> SEQ ID NO: 1
     17 <211> LENGTH: 337
     18 <212> TYPE: PRT
     19 <213> ORGANISM: rat
    20 <400> SEQUENCE: 1
    21
              Met Val Cys Val Leu Arg Asp Thr Thr Gly Arg Phe Val Ser Met Asp
    22
                                                   10
    23
              Pro Thr Ile Ser Ser Leu Ser Thr Glu Ser Thr Thr Leu Asn Lys Thr
    24
                                               25
    25
              Gly His Pro Ser Cys Arg Pro Ile Leu Thr Leu Ser Phe Leu Val Pro
    26
    27
              Ile Ile Thr Leu Leu Gly Leu Ala Gly Asn Thr Ile Val Leu Trp Leu
    28
    29
              Leu Gly Phe Arg Met Arg Arg Lys Ala Ile Ser Val Tyr Val Leu Asn
    30
                                  70
                                                       75
    31
              Leu Ser Leu Ala Asp Ser Phe Phe Leu Cys Cys His Phe Ile Asp Ser
    32
                              85
                                                   90
    33
              Leu Met Arg Ile Met Asn Phe Tyr Gly Ile Tyr Ala His Lys Leu Ser
    34
                                               105
    35
              Lys Glu Ile Leu Gly Asn Val Ala Phe Ile Pro Tyr Ile Ser Gly Leu
    36
                                           120
    37
              Ser Ile Leu Ser Ala Ile Ser Thr Glu Arg Cys Leu Ser Val Leu Trp
    38
                                      135
                                                           140
    39
              Pro Ile Trp Tyr His Cys His Arg Pro Arg Asn Met Ser Ala Ile Ile
    40
                                  150
    41
              Cys Val Leu Ile Trp Val Leu Ser Phe Leu Met Gly Ile Leu Asp Trp
    42
                              165
                                                   170
    43
              Phe Phe Ser Gly Phe Leu Gly Glu Thr His His His Leu Trp Lys Asn
    44
                          180
                                               185
                                                                   190
```

```
45
         Val Asp Phe Ile Val Thr Ala Phe Leu Ile Phe Leu Phe Met Leu Leu
46
                 195
                                      200
47
         Phe Gly Ser Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg
48
                                  215
49
         Arg Lys Pro Leu Ser Arg Leu Tyr Val Thr Ile Ser Leu Thr Val Met
50
                              230
                                                  235
51
         Val Tyr Leu Ile Cys Gly Leu Pro Leu Gly Leu Tyr Leu Phe Leu Leu
52
                          245
                                              250
53
         Tyr Trp Phe Gly Ile His Leu His Tyr Pro Phe Cys His Ile Tyr Gln
54
                                          265
                                                               270
55
         Val Thr Val Leu Leu Ser Cys Val Asn Ser Ser Ala Asn Pro Ile Ile
56
                                      280
57
         Tyr Phe Leu Val Gly Ser Phe Arg His Arg Lys Lys His Arg Ser Leu
58
                                  295
                                                      300
59
         Lys Met Val Leu Lys Arg Ala Leu Glu Glu Thr Pro Glu Glu Asp Glu
60
                              310
                                                  315
61
         Tyr Thr Asp Ser His Val Gln Lys Pro Thr Glu Ile Ser Glu Arg Arg
62
                                              330
                         325
63
         Cys
65 <210> SEQ ID NO: 2
66 <211> LENGTH: 1011
67 <212> TYPE: DNA
68 <213> ORGANISM: rat
69 <400> SEQUENCE: 2
70
         atggtttgtg ttctcaggga cactactgga agatttgtga gcatggatcc aaccatctca
                                                                                 60
71
         teceteagta cagaatetae aacaetgaat aaaaetggte ateceagttg caggecaate
                                                                                120
72
         ctcaccctgt ccttcctggt ccccatcatc accctgcttg gattggcagg aaacaccatt
                                                                                180
73
         gtactctggc tcttgggatt ccgcatgcgc aggaaagcca tctcagtcta cgtcctcaac
                                                                                240
         ctgtctctgg cagactcctt cttcctctgc tgccatttta ttgactctct gatgcggatc
                                                                                300
75
         atgaacttct atggcatcta tgcccataaa ttaagcaaag aaatcttagg caatgtagca
                                                                                360
76
         tteatteect atateteagg cetgageate eteagtgeta teageaegga gegetgeetg
                                                                                420
77
         tetgtattgt ggccaatetg gtaccaetge caeegeccaa gaaacatgte agetattata
                                                                                480
78
         tgtgttctaa tctgggttct gtcctttctc atgggcatcc ttgactggtt tttctcagga
                                                                                540
79
         ttcctgggtg agactcacca tcatttgtgg aaaaatgttg actttattgt aactgcattt
                                                                                600
80
         etgatttttt tatttatget tetetttggg teeagtetgg egetaetggt gaggateete
                                                                                660
81
         tgtggttcca gacggaaacc actgtccagg ctgtacgtta caatctctct cacagtgatg
                                                                                720
82
         gtctacctca tctgcggcct gcctctcggg ctttacttgt tcctgctata ttggtttggg
                                                                                780
83
         atcoatttac attatecett ttgteacatt taccaagtta etgtgeteet gteetgtgtg
                                                                                840
84
         aacagctctg ccaaccccat catttacttc cttgtagggt cctttaggca ccgtaaaaag
                                                                                900
85
         categgteee teaaaatggt tettaaaagg getetggagg agaeteetga ggaggatgaa
                                                                                960
         tatacagaca gccatgttca gaaacccact gagatctcag aaaggagatg t
                                                                               1011
88 <210> SEQ ID NO: 3
89 <211> LENGTH: 322
90 <212> TYPE: PRT
91 <213> ORGANISM: Homo sapiens
92 <400> SEQUENCE: 3
93
         Met Asp Pro Thr Ile Pro Val Leu Gly Thr Lys Leu Thr Pro Ile Asn
94
                                              10
95
         Gly Arg Glu Glu Thr Pro Cys Tyr Asn Gln Thr Leu Ser Phe Thr Gly
```

96					20					25					30			
97		Leu	Thr	Cys	Ile	Ile	Ser	Leu	Val	Ala	Leu	Thr	Gly	Asn	Ala	Val	Val	
98				35					40				_	45				
99		Leu	Trp	Leu	Leu	Gly	Cys	Arg	Met	Arg	Arg	Asn	Ala	Val	Ser	Ile	Tyr	
100			50					55		_			60				_	
101		Ile	Leu	Asr	Leu	ı Val	. Ala	Ala	Asn	Phe	Leu	ı Phe	Let	ı Ser	Gly	His	: Ile	
102		65					70					75					80	
103		Ile	Phe	Ser	Pro	Lev	Pro	Leu	Ile	Asr	ılle	Arg	His	Pro	Ile	Ser	Lys	
104						85					90					95		
105		Ile	Let	Ser	Pro	Val	Met	Thr	Phe	Pro	Tyr	Phe	Ile	e Gly	Leu	Ser	Met	
106					100)				105	5				110)		
107		Leu	Ser	Ala	Ile	e Ser	Thr	Glu	Arg	Cys	Leu	Ser	Ile	Leu	Trp	Pro	Ile	
108				115					120					125				
109		Trp	Tyr	His	Cys	Arg	, Arg	Pro	Arg	Tyr	Leu	Ser	Sei	: Val	Met	Cys	: Val	
110			130)				135					140)				
111		Leu	Let	Trp) Ala	i Leu	Ser	Leu	Leu	Arg	Ser	: Ile	Let	ı Glu	Trp	Met	Phe	
112		145					150					155					160	
113		Cys	Asp	Phe	Let	ı Phe	Ser	Gly	Ala	Asn	Ser	· Val	Trp	Cys	Glu	Thr	Ser	
114						165	;				170)				175	•	•
115		Asp	Phe	lle	Thr	: Ile	Ala	Trp	Leu	Val	Phe	Leu	Суя	: Val	Val	. Lev	Cys	
116					180					185					190			
117		Gly	Ser			ı Val	. Leu	Leu		_	Ile	Leu	Cys			Arg	Lys	
118			_	195					200		_			205			_	
119		Met			Thr	Arg	Leu	Tyr		Thr	· Ile	Leu			. Val	Leu	. Val	
120		51. .	210		_	~1	_	215		~7	~ 7	~7	220		_	-1	_	
121				Leu	Cys	s Gry		Pro	Phe	GIY	TIE		_) Ala	Leu	Pne		
122		225		774		. 7	230		77-7	T	Dh.	235			***		240	
123		Arg	116	HIS	ь тел	_	_	Lys	vaı	ьеи		_	HIS	s var	HIS			
124 125		Cor	Tlo	Dho		245		T 011	7 0 0	Cox	250		7.00	. Dro		255		
126		PET	116	FILE	260		ATO	Leu	ASII	265		Ата	ASI	PIO	270		TYL	
127		Phe	Phe	Val			Phe	Arg	Gln			Δgn	Δτο	r Gln			Lve	
128		2110	1110	275	_	DCI	1110	my	280	_	, GIII	, ASI	. AL	285		, neu	. шуз	
129		Leu	Val			a Ara	Ala	Leu			Thr	Pro	Glu			Glu	Gly	
130			290			3	,	295	0				300				. 0-1	
131		Gly			Leu	Pro	Gln	Glu	Thr	Leu	Glu	Leu			Ser	Lvs	Leu	
132		305					310					315		1		-1-	. 320	
133			Gln	ļ														
135 <2	210>				4													
136 <2																		
137 <2																		
138 <2	213>	ORG	ANIS	м: н	omo	sapi	ens											
139 <4						-												
140		atg	gato	caa	ccat	ccca	gt c	ttgg	gtac	a aa	actg	acac	caa	itcaa	cgg	acgt	gaggag	g 60
141																	cttgto	
142																	aacgct	
143																	cacatt	
144		ata	tttt	cgc	cgtt	accc	ct c	atca	atat	c cg	ccat	ccca	tct	ccaa	aat	cctc	agtcct	300
145		gtg	atga	cct	ttcc	ctac	tt t	atag	gcct	a ag	catg	ctga	gcg	ccat	cag	cacc	gagcgc	360

146		tgc	ctgt	cca 1	tcct	gtgg	CC C	atct	ggtad	c cad	ctgc	cgcc	gcc	ccaga	ata d	cctg	tcatcg	42	0
147																	atgttc	48	0
148		tgt	gacti	tcc 1	tgtti	tagt	gg t	gctaa	attci	t gti	tggt	tgtg	aaa	cgtc	aga 1	tttca	attaca	54	
149		-											-	_		_	ctggtc	60	
150		agga	attci	tct q	gtgg	atcc	cg ga	aagat	tgcc	g ct	gacca	aggc	tgta	acgt	gac (catc	ctcctc	66	0
151		acag	gtgci	tgg 1	tctt	cctc	ct c	tgtg	gcct	g cc	cttt	ggca	ttca	agtg	ggc (cctgi	ttttcc	72	0
152		agga	atcca	acc 1	tggai	ttgga	aa a	gtcti	tatti	t tgi	cate	gtgc	atc	tagti	ttc	catti	ttcctg	78	0
153		tcc	gctc	tta a	acag	cagt	ge ea	aacc	ccat	c att	tact	ttct	tcgi	tggg	ctc (cttta	aggcag	84	0
154		cgt	caaaa	ata 🤉	ggca	aaac	ct ga	aagct	tggti	cto	ccaa	aggg	ctc	tgca	gga (cacgo	cctgag	90	0
155		gtg	gatga	aag g	gtgg	aggg	tg go	cttc	ctcag	g gaa	aacco	ctgg	agct	tgtc	ggg a	aagca	aaattg	96	0
156		gage	cagt	ga														96	9
158	<210>	SEQ	ID I	NO:	5														
159	<211>	LEN	GTH:	322															
160	<212>	TYP	E: PI	RT															
161	<213>	ORG	ANISI	M: H	omo :	sapi	ens												
162	<400>	SEQ	JENCI	E: 5															
163		Met	Asp	Pro	Thr	Val	Pro	Val	Leu	Gly	Thr	Glu	Leu	Thr	Pro	Ile	Asn		
164		1				5					10					15			
165		Gly	Arg	Glu	Glu	Thr	Pro	Cys	Tyr	Lys	Gln	Thr	Leu	Ser	Phe	Thr	Gly		
166					20					25					30				
167		Leu	Thr	Cys	Ile	Val	Ser	Leu	Val	Ala	Leu	Thr	Gly	Asn	Ala	Val	Val		
168				35					40					45					
169		Leu	Trp	Leu	Leu	Gly	Cys	Arg	Met	Arg	Arg	Asn	Ala	Val	Ser	Ile	Tyr		
170			50					55					60						
171		Ile	Leu	Asn	Leu	Val	Ala	Ala	Asp	Phe	Leu	Phe	Leu	Ser	Gly	His	Ile		
172		65					70					75					80		
173		Ile	Cys	Ser	Pro	Leu	Arg	Leu	Ile	Asn	Ile	Ser	His	Pro	Ile	Ser	Lys		
174						85					90					95			
175		Ile	Leu	Ser		Val	Met	Thr	Phe	Pro	Tyr	Phe	Ile	Gly	Leu	Ser	Met		
176					100					105			_		110		_		
177		Leu	Asn		Ile	Ser	Thr	Glu	_	Cys	Leu	Ser	Ile		\mathtt{Trp}	Pro	Ile		
178				115					120					125			_		
179		Trp		His	Cys	Arg	Arg		Arg	Tyr	Leu	Ser		Val	Met	Cys	Val		
180			130		_			135					140						
181			Leu	Trp	Ala	Pro		Leu	Leu	Arg	Ser		Leu	Glu	Trp	Met			
182		145	_				150				_	155	_	_			160		
183		Cys	Asp	Phe	Leu		Ser	Gly	Ala	Asp		Val	Arg	Cys	Glu	Thr	Ser		
184		_				165		_	_		170	_	_			175			
185		Asp	Phe	Ile		Ile	Ala	Trp	Leu		Phe	Leu	Arg	Val		Leu	Cys		
186			Δ	_	180		_	_		185		_	_		190		_		
187		Gly	Ser		Leu	Val	Leu	Leu		Arg	Ile	Leu	Cys		Ser	Arg	Lys		
188				195					200		Δ			205	$\bigcap_{}$				
189		Met		Leu	Thr	Arg	Leu	_	Val	Thr	Ile	Leu		Thr	Val	Leu	Val		
190			210					215					220				_		
191			Leu	Leu	Cys	Gly		Pro	Phe	Gly	Ile		Trp	Ala	Leu	Phe			
192		225					230			_ ^		235				_	240		
193		Arg	Ile	His	Leu	_	Trp	Lys	Val	Leu		Cys	His	Val	His	Leu	Val		
194						245			_		250		_			255	_		
195		Ser	Ile	Phe	Leu	Ser	Ala	Leu	Asn	Ser	Ser	Ala	Asn	Pro	Ile	Ile	Tyr		

196	260 265 270
197	Phe Phe Met Gly Ser Phe Arg Gln Leu Gln Asn Arg Lys Thr Leu Lys
198	275 280 285
199	Leu Val Leu Gln Arg Asp Leu Gln Asp Thr Pro Glu Val Asp Glu Gly
200	290 295 300 .
201	Gly Trp Trp Leu Pro Gln Glu Thr Leu Glu Leu Ser Gly Ser Lys Leu
202	305 310 315 320
203	Glu Ile
	SEQ ID NO: 6
	LENGTH: 969
	TYPE: DNA
	ORGANISM: Homo sapiens
	SEQUENCE: 6
210	atggatecaa cegteccagt ettgggtaca gaactgacae caatcaaegg aegtgaggag 60
211	actecttget acaagcagac cetgagette aeggggetga egtgeategt ttecettgte 120
212	gegetgacag gaaacgeggt tgtgetetgg etectggget geegeatgeg caggaacget 180
213	
213	gtctccatct acatcctcaa cctggtcgcg gccgacttcc tcttccttag cggccacatt 240 atatgttcgc cgttacgcct catcaatatc agccatccca tctccaaaat cctcagtcct 300
215	gtgatgacct ttccctactt tataggccta agcatgctga acgccatcag caccgagcgc 360
216	tgcctgtcca tcctgtggcc catctggtac cactgccgcc gccccagata cctgtcatcg 420
217	gtcatgtgtg tcctgctctg ggccccgtcc ctgctgcgga gtatcctgga gtggatgttc 480
218	tgtgacttcc tgtttagtgg tgctgattct gttcggtgtg aaacgtcaga tttcattaca 540
219	atcgcgtggc tggtttttt acgtgtggtt ctctgtgggt ccagcctggt cctgctggtc 600
220	aggattetet gtggateeeg gaagatgeeg etgaceagge tgtaegtgae cateeteete 660
221	acagtgctgg tetteeteet etgtggeetg eeetttggea tteagtggge eetgtttee 720
222	aggatccacc tggattggaa agtcttattt tgtcatgtgc atctagtttc cattttcctg 780
223	tccgctctta acagcagtgc caaccccatc atttacttct tcatgggctc ctttaggcag 840
224	cttcaaaaca ggaagaccct caagctggtt ctccagaggg atctgcagga cacgcctgag 900
225	gtggatgaag gtggatggtg gcttcctcag gaaaccctgg agctgtcggg aagcaaattg 960
226	gagatetga 969
	SEQ ID NO: 7
	LENGTH: 322
	TYPE: PRT
	ORGANISM: Homo sapiens
	SEQUENCE: 7
233	Met Asp Pro Thr Val Ser Thr Leu Asp Thr Glu Leu Thr Pro Ile Asn
234	1 5 10 15
235	Gly Thr Glu Glu Thr Leu Cys Tyr Lys Gln Thr Leu Ser Leu Thr Val
236	20 25 30
237	Leu Thr Cys Ile Val Ser Leu Val Gly Leu Thr Gly Asn Ala Val Val
238	35 40 45
239	Leu Trp Leu Leu Gly Cys Arg Met Arg Arg Asn Ala Phe Ser Ile Tyr
240	50 55 60
241	Ile Leu Asn Leu Ala Ala Ala Asp Phe Leu Phe Leu Ser Gly Arg Leu
242	65 70 75 80
243	Ile Tyr Ser Leu Leu Ser Phe Ile Ser Ile Pro His Thr Ile Ser Lys
244	85
245	Ile Leu Tyr Pro Val Met Met Phe Ser Tyr Phe Ala Gly Leu Asn Phe
246	100 105 110

Input Set : N:\Crf3\RULE60\10747702.raw.txt
Output Set: N:\CRF4\10062005\J747702.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 25,28,31,34

Seq#:16; N Pos. 10,13

11

VERIFICATION SUMMARYDATE: 10/07/2005PATENT APPLICATION: US/10/747,702TIME: 12:54:21

Input Set : N:\Crf3\RULE60\10747702.raw.txt
Output Set: N:\CRF4\10062005\J747702.raw

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0 L:528 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0